

0280

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ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/756,247

DATE: 01/25/2001

TIME: 10:36:26

Input Set : A:\es.txt

Output Set: N:\CRF3\01252001\I756247.raw

3 <110> APPLICANT: Godbole, Shubhada D
4 Boyle, Bryan J
5 Mize, Nancy K
6 Deng, Cenhua
7 Goodrich, Ryle
8 Arterburn, Matthew C
9 Zhou, Ping
10 Tang, Y. Tom
11 Liu, Chenghua
12 Yeung, George
13 Drmanac, Radoje T
15 <120> TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDES
16 AND POLYNUCLEOTIDES
18 <130> FILE REFERENCE: HYS-31CIP
C--> 20 <140> CURRENT APPLICATION NUMBER: US/09/756,247
21 <141> CURRENT FILING DATE: 2001-01-08
23 <150> PRIOR APPLICATION NUMBER: 09/649,167
24 <151> PRIOR FILING DATE: 2000-08-23
26 <150> PRIOR APPLICATION NUMBER: 09/540,217
27 <151> PRIOR FILING DATE: 2000-03-31
29 <150> PRIOR APPLICATION NUMBER: 09/684,711
30 <151> PRIOR FILING DATE: 2000-10-06
32 <150> PRIOR APPLICATION NUMBER: 09/560,875
33 <151> PRIOR FILING DATE: 2000-04-27
35 <150> PRIOR APPLICATION NUMBER: 09/196,914
36 <151> PRIOR FILING DATE: 2000-02-03
38 <160> NUMBER OF SEQ ID NOS: 41
40 <170> SOFTWARE: PatentIn version 3.0
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45 <213> ORGANISM: Homo sapiens
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52 cttccaactg gcaccagagg caatgctgga cactacatg tggcagtggc tgagggcaag 180
54 acctttggtt ctttcagtgt ggagggaatat gtgctgccga agtttaaggga ggatttcgtc 240
56 cacaatccgg gggcggggag taggaattat tttttgcttt gaggagaaca aaaaggttct 300
58 aattcagagg ggggaacggca ctttgtaca gactgacaaa cctctctaca ccccgaggca 360
60 gcaagtgatc ttccgcattg tcacca 386
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75 gaacggcacc ttgtacaga ctgacaaaacc tctctacacc ccagggcagc aagtgtattt 240
77 ccgcattgtc accatggata gcaacttcgt tccagtgaat gacaagtact ccatggtgga 300
79 actacaggat ccaaatagca acaggattgc acagtggctg gaagtggtag ctgagcaagg 360
81 cattgtagac ctgtccttcc aactggcacc agaggcaatg ctgggcacct acactgtggc 420
83 agtggctgag ggcaagacct ttggtacttt cagtgtggag gaatatgtgc tgcggaagtt 480
85 taaggtggaa gtgttggaac ccaaggagt atcaacggtg caggaatcct tcttagttaa 540
87 aattttgtgt aggtacacct atggaaaagg catgctaggg gcagtgcagg tatctgtgtg 600
89 tcagaagggc aaatacttac tggatctgag aggtgggaac gggaaccagc ttcctggacc 660
91 aatgcaggaa cctctctgga cagactgaca aaacaggatg ttctctagca cctgtggaca 720
93 tggccacctt tgacctcatt ggaatagcgt acagccatca aatcaatatt gtggctactg 780
95 ttgtggagga agggacaggt gtggaggcca atgccactca gaatatctac atttctccac 840
97 aaatgggatt aaatgacctt tggaaagcac cagcaatttt taccatccaa attttccct 900
99 tcagtgggga agataaggaa ttaqggggcca atgatgacct ctctctcaag aaccatctag 960
101 tgtttctggg qatttatggc acaaatggaa ccttcaacca gacctggtt actgataaca 1020
103 atggcctagc tccctttacc ttggaagaaa tccccggtg aaagggacag aacgttctct 1080
105 ggagggaagg ttttcaatag gaaaacttat tatataatcc ggaacaaaag gccaccgta 1140
107 ctacaaaaaa ggcctaacct gggcctgcga acccttttac aagaacaaac ccggaacttl 1200
109 cctttggcat tccccggtt taaacggccc cttgaaatgt ggcagcccc aggaagtgt 1260
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128 1 5 10 15
130 gca gaa gaa ctt cca aac tac ctg gtg aca tta cca gcc egg cta aat 96
131 Ala Glu Glu Leu Pro Asn Tyr Leu Val Thr Leu Pro Ala Arg Leu Asn
132 20 25 30
134 ttc ccc tcc gtt cag aag gtt tgt ttg gac ctg agc cct ggg tac aqt 144
135 Phe Pro Ser Val Gln Lys Val Cys Leu Asp Leu Ser Pro Gly Tyr Ser
136 35 40 45
138 gat gtt aaa ttc acg gtt act ctg gag acc aag gac aag acc cag aag 192
139 Asp Val Lys Phe Thr Val Thr Leu Glu Thr Lys Asp Lys Thr Gln Lys
140 50 55 60
142 ttg cta gaa tac tct gga ctg aag aag agg cac tta cat tgt atc tcc 240
143 Leu Leu Glu Tyr Ser Gly Leu Lys Lys Arg His Leu His Cys Ile Ser
144 65 70 75 80
146 ttt ctt gta cca cct cct gct ggt ggc aca gaa gtg gcc aca atc 288
147 Phe Leu Val Pro Pro Pro Ala Gly Gly Thr Glu Glu Val Ala Thr Ile
148 85 90 95
150 cgg gtg tgg gga gtt gga aat aac atc agc ttt gag gag aag aaa aag 336
151 Arg Val Ser Gly Val Gly Asn Asn Ile Ser Phe Glu Glu Lys Lys Lys

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Input Set : A:\es.txt
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155 Val Leu Ile Gln Arg Gln Gly Asn Gly Thr Phe Val Gln Thr Asp Lys				
156 115 120 125				
158 cct ctc tac acc cca ggg cag caa gtg tat ttc cgc att gtc acc atg	432			
159 Pro Leu Tyr Thr Pro Gly Gln Gln Val Tyr Phe Arg Ile Val Thr Met				
160 130 135 140				
162 gat agc aac ttc gtt cca gtg aat gac aag tac tcc atg gtg gaa cta	480			
163 Asp Ser Asn Phe Val Pro Val Asn Asp Lys Tyr Ser Met Val Glu Leu				
164 145 150 155 160				
166 cag gat cca aat agc aac agg att gca cag tgg ctg gaa gtg gta cct	528			
167 Gln Asp Pro Asn Ser Asn Arg Ile Ala Gln Trp Leu Glu Val Val Pro				
168 165 170 175				
170 gag caa ggc att gta gac ctg tcc ttc caa ctg gca cca gag gca atg	576			
171 Glu Gln Gly Ile Val Asp Leu Ser Phe Gln Leu Ala Pro Glu Ala Met				
172 180 185 190				
174 ctg ggc acc tac act gtg gca gtg gct gag ggc aag acc ttt ggt act	624			
175 Leu Gly Thr Tyr Thr Val Ala Val Ala Glu Gly Lys Thr Phe Gly Thr				
176 195 200 205				
178 ttc aqt gtg gag gaa tat gtg ctg ccg aag ttt aag gtg gaa gtg gtg	672			
179 Phe Ser Val Glu Glu Tyr Val Leu Pro Lys Phe Lys Val Glu Val Val				
180 210 215 220				
182 gaa ccc aag gag tta tca acg gtg cag gaa tct ttc tta gta aaa att	720			
183 Glu Pro Lys Glu Leu Ser Thr Val Gln Glu Ser Phe Leu Val Lys Ile				
184 225 230 235 240				
186 tgt tgt agg tac acc tat gga aag ccc atg cta ggg gca gtg cag gta	768			
187 Cys Cys Arg Tyr Thr Tyr Gly Lys Pro Met Leu Gly Ala Val Gln Val				
188 245 250 255				
190 tct gtg tgt cag aag gca aat act tac tgg tat cga gag gtg gaa cgg	816			
191 Ser Val Cys Gln Lys Ala Asn Thr Tyr Trp Tyr Arg Glu Val Glu Arg				
192 260 265 270				
194 gaa cag ctt cct gac aaa tgc agg aac ctc tct qqa cag act gac aaa	864			
195 Glu Gln Leu Pro Asp Lys Cys Arg Asn Leu Ser Gly Gln Thr Asp Lys				
196 275 280 285				
198 aca gga tgt ttc tca gca cct gtg gac atg gcc acc ttt gac ctc att	912			
199 Thr Gly Cys Phe Ser Ala Pro Val Asp Met Ala Thr Phe Asp Leu Ile				
200 290 295 300				
202 gga tat gcg tac agc cat caa atc aat att gtg gct act gtt gtg gag	960			
203 Gly Tyr Ala Tyr Ser His Gln Ile Asn Ile Val Ala Thr Val Val Glu				
204 305 310 315 320				
206 gaa ggg aca ggt gtg gag gcc aat gcc act cag aat atc tac att tct	1008			
207 Glu Gly Thr Gly Val Glu Ala Asn Ala Thr Gln Asn Ile Tyr Ile Ser				
208 325 330 335				
210 cca caa atg gga tca atg acc ttt gaa gac acc agc aat ttt tac cat	1056			
211 Pro Gln Met Gly Ser Met Thr Phe Glu Asp Thr Ser Asn Phe Tyr His				
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216 355 360 365				

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220		370					375				380						
222	gga	acc	ttc	aac	cag	acc	ctg	gtt	act	gat	aac	aat	ggc	cta	gct	ccc	1200
223	Gly	Thr	Phe	Asn	Gln	Thr	Leu	Val	Thr	Asp	Asn	Asn	Gly	Leu	Ala	Pro	
224	385					390					395				400		
226	ttt	acc	ttg	gag	aca	tcc	ggt	tgg	aat	ggg	aca	gac	gtt	tct	ctg	gag	1248
227	Phe	Thr	Leu	Glu	Thr	Ser	Gly	Trp	Asn	Gly	Thr	Asp	Val	Ser	Leu	Glu	
228				405					410					415			
230	gga	aag	ttt	caa	atg	gaa	gac	tta	gta	tat	aat	ccg	gaa	caa	gtg	cca	1296
231	Gly	Lys	Phe	Gln	Met	Glu	Asp	Leu	Val	Tyr	Asn	Pro	Glu	Gln	Val	Pro	
232			420					425					430				
234	cgt	tac	tac	caa	aat	gcc	tac	ctg	cac	ctg	cga	ccc	ttc	tac	agc	aca	1344
235	Arg	Tyr	Tyr	Gln	Asn	Ala	Tyr	Leu	His	Leu	Arg	Pro	Phe	Tyr	Ser	Thr	
236			435				440						445				
238	acc	cgc	agc	ttc	ctt	ggc	atc	cac	cgg	cta	aac	ggc	ccc	ttg	aaa	tgt	1392
239	Thr	Arg	Ser	Phe	Leu	Gly	Ile	His	Arg	Leu	Asn	Gly	Pro	Leu	Lys	Cys	
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242	ggc	cag	ccc	cag	gaa	gtg	ctg	gtg	gat	tat	tac	atc	gac	ccg	gcc	gat	1440
243	Gly	Gln	Pro	Gln	Glu	Val	Leu	Val	Asp	Tyr	Tyr	Ile	Asp	Pro	Ala	Asp	
244	465				470				475				480				
246	gca	agc	cct	gac	caa	gag	atc	agc	ttc	tcc	tac	tat	tta	ata	ggg	aaa	1488
247	Ala	Ser	Pro	Asp	Gln	Glu	Ile	Ser	Phe	Ser	Tyr	Tyr	Leu	Ile	Gly	Lys	
248				485					490				495				
250	gga	agt	ttg	gtg	atg	gag	ggg	caq	aaa	cac	ctg	aac	tct	aag	aaq	aaa	1536
251	Gly	Ser	Leu	Val	Met	Glu	Gly	Gln	Lys	His	Leu	Asn	Ser	Lys	Lys	Lys	
252			500				505						510				
254	gga	ctg	aaa	gcc	tcc	ttc	tct	ctc	tca	ctg	acc	ttc	act	tcg	aga	ctg	1584
255	Gly	Leu	Lys	Ala	Ser	Phe	Ser	Leu	Ser	Leu	Thr	Phe	Thr	Ser	Arg	Leu	
256		515				520						525					
258	gcc	cct	gat	cct	tcc	ctg	gtg	atc	tat	gcc	att	ttt	ccc	agt	gga	ggt	1632
259	Ala	Pro	Asp	Pro	Ser	Leu	Val	Ile	Tyr	Ala	Ile	Phe	Pro	Ser	Gly	Gly	
260		530				535						540					
262	gtt	gta	gct	gac	aaa	att	cag	ttc	tca	gtc	ggg	atg	tgc	ttt	gac	aat	1680
263	Val	Val	Ala	Asp	Lys	Ile	Gln	Phe	Ser	Val	Gly	Met	Cys	Phe	Asp	Asn	
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266	cag	gtt	tcc	ctt	ggc	ttc	tcc	ccc	tcc	cag	cag	ctt	cca	gga	gca	gaa	1728
267	Gln	Val	Ser	Leu	Gly	Phe	Ser	Pro	Ser	Gln	Glu	Leu	Pro	Gly	Ala	Glu	
268			565					570					575				
270	gtg	gag	ctg	cag	ctg	cag	gca	gct	ccc	gga	tcc	ctg	tgt	gcg	ctc	cgg	1776
271	Val	Glu	Leu	Gln	Leu	Gln	Ala	Ala	Pro	Gly	Ser	Leu	Cys	Ala	Leu	Arg	
272			580				585						590				
274	gcg	gtg	gat	gag	agt	gtc	tta	ctg	ctt	agg	cca	gac	aga	gag	ctg	agc	1824
275	Ala	Val	Asp	Glu	Ser	Val	Leu	Leu	Leu	Arg	Pro	Asp	Arg	Glu	Leu	Ser	
276			595				600					605					
278	aac	cgc	tct	gtc	tat	ggg	atg	ttt	cca	ttc	tgg	tat	ggt	cac	tac	ccc	1872
279	Asn	Arg	Ser	Val	Tyr	Gly	Met	Phe	Pro	Phe	Trp	Tyr	Gly	His	Tyr	Pro	
280		610				615						620					
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287	Phe	Pro	Gln	Pro	Leu	Ile	Asp	Pro	Met	Pro	Gln	Gly	His	Ser	Ser	Gln	
288					645					650					655		
290	cgt	tcc	att	atc	tgg	agg	ccc	tcg	ttc	tct	gaa	ggc	acg	gac	ctt	ttc	2016
291	Arg	Ser	Ile	Ile	Trp	Arg	Pro	Ser	Phe	Ser	Glu	Gly	Thr	Asp	Leu	Phe	
292					660					665					670		
294	agc	ttt	tcc	cgg	gac	gtg	ggc	ctg	aaa	ata	ctg	tcc	aat	gcc	aaa	atc	2064
295	Ser	Phe	Phe	Arg	Asp	Val	Gly	Leu	Lys	Ile	Leu	Ser	Asn	Ala	Lys	Ile	
296			675				680							685			
298	aag	aag	cca	gta	gat	tgc	aqt	cac	aga	tct	cca	gaa	tac	agc	act	gct	2112
299	Lys	Lys	Pro	Val	Asp	Cys	Ser	His	Arg	Ser	Pro	Glu	Tyr	Ser	Thr	Ala	
300			690				695					700					
302	atg	ggt	ggc	ggt	ggt	cat	cca	qag	gct	ttt	gag	tca	tca	act	cct	tta	2160
303	Met	Gly	Gly	Gly	Gly	Pro	Glu	Ala	Phe	Glu	Ser	Ser	Thr	Pro	Leu		
304	705					710						715			720		
306	cat	caa	gca	gag	gat	tct	cag	gtc	cgc	cag	tac	tcc	cca	gag	acc	tgg	2208
307	His	Gln	Ala	Glu	Asp	Ser	Gln	Val	Arg	Gln	Tyr	Phe	Pro	Glu	Thr	Trp	
308					725					730					735		
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311	Leu	Trp	Asp	Leu	Phe	Pro	Ile	Gly	Asn	Ser	Gly	Lys	Glu	Ala	Val	His	
312			740						745					750			
314	gtc	aca	gtt	cct	gac	gcc	atc	acc	gag	tgg	aag	gcg	atg	agt	ttc	tgc	2304
315	Val	Thr	Val	Pro	Asp	Ala	Ile	Thr	Glu	Trp	Lys	Ala	Met	Ser	Phe	Cys	
316			755				760						765				
318	act	tcc	cag	tca	aga	ggc	tcc	ggg	ctt	tca	ccc	act	gtt	gga	cta	act	2352
319	Thr	Ser	Gln	Ser	Arg	Gly	Phe	Gly	Leu	Ser	Pro	Thr	Val	Gly	Leu	Thr	
320			770				775					780					
322	gct	ttc	aag	cgg	tcc	ttt	gtt	gac	ctg	act	ctc	cct	tac	tca	gta	gtc	2400
323	Ala	Phe	Lys	Pro	Phe	Phe	Val	Asp	Leu	Thr	Leu	Pro	Tyr	Ser	Val	Val	
324	785					790						795			800		
326	cgt	ggg	gaa	tcc	ttt	cgt	ctt	act	gcc	acc	atc	tcc	aat	tac	cta	aag	2448
327	Arg	Gly	Glu	Ser	Phe	Arg	Leu	Thr	Ala	Thr	Ile	Phe	Asn	Tyr	Leu	Lys	
328					805					810				815			
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331	Asp	Cys	Ile	Arg	Val	Gln	Thr	Asp	Leu	Ala	Lys	Ser	His	Glu	Tyr	Gln	
332				820					825					830			
334	cta	gaa	tca	tgg	gca	gat	tct	cag	acc	tcc	agt	tgt	ctc	tgt	gct	gat	2544
335	Leu	Glu	Ser	Trp	Ala	Asp	Ser	Gln	Thr	Ser	Ser	Cys	Leu	Cys	Ala	Asp	
336			835						840					845			
338	gac	gca	aaa	acc	cac	cac	tgg	aac	atc	aca	gct	gtc	aaa	tty	ggt	cac	2592
339	Asp	Ala	Lys	Thr	His	His	Trp	Asn	Ile	Thr	Ala	Val	Lys	Leu	Gly	His	
340		850					855					860					
342	att	aac	ttt	act	att	agt	aca	aag	att	ctg	gac	agc	aat	gaa	cca	tgt	2640
343	Ile	Asn	Phe	Thr	Ile	Ser	Thr	Lys	Ile	Leu	Asp	Ser	Asn	Glu	Pro	Cys	
344	865					870					875				880		
346	ggg	ggc	cag	aag	ggg	ttt	gtt	ccc	caa	aag	ggc	cga	agt	gac	acg	ctc	2688
347	Gly	Gly	Gln	Lys	Gly	Phe	Val	Pro	Gln	Lys	Gly	Arg	Ser	Asp	Thr	Leu	

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:20 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26